

Resource Summary Report

Generated by [RRID](#) on Aug 12, 2026

d-StructMAn

RRID:SCR_022534

Type: Tool

Proper Citation

d-StructMAn (RRID:SCR_022534)

Resource Information

URL: <https://github.com/kalininalab/d-StructMAn>

Proper Citation: d-StructMAn (RRID:SCR_022534)

Description: Software tool provides annotation of non-synonymous single nucleotide variants in context of structural properties of resulting amino acid changes in corresponding proteins. Improved implementation of StructMAn, shipped in container form and extended to annotation of short in-frame indels and alterations arising as consequence of alternative splicing events. Produces range of structural features by combining information from experimentally resolved structures of many related proteins, which is unique feature of StructMAn family tools. Can also harness all protein structure models stored in AlphaFold Protein Structure Database.

Abbreviations: d-StructMAn

Synonyms: d-Structural Mutation Annotation

Resource Type: software application, software resource

Keywords: Structural mutation annotation, non-synonymous single nucleotide variants annotation, non-synonymous single nucleotide variants, structural properties, amino acid changes, protein structure

Availability: Free, Available for download, Freely available

Resource Name: d-StructMAn

Resource ID: SCR_022534

License: GNU Lesser General Public License v2.1

Record Creation Time: 20220707T050149+0000

Record Last Update: 20260810T040824+0000

Ratings and Alerts

No rating or validation information has been found for d-StructMAn.

No alerts have been found for d-StructMAn.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 1 mentions in open access literature.

Listed below are recent publications. The full list is available at [RRID](#) .

Gress A, et al. (2022) d-StructMAn: Containerized structural annotation on the scale from genetic variants to whole proteomes. GigaScience, 11.